We claim:

1. A method for mapping a gene network comprising the steps of:

preparing a plurality of biological samples;

detecting and comparing the expression of at least 5 genes in said biological samples;

generating a cluster map for said genes according to the correlation in expression among said genes; and

analyzing said cluster map to generate gene network causal models defining regulatory relationships among said genes.

2. The method of claim 1, wherein expression of said genes is detected by measuring the relative and/ or absolute amount of transcripts of said genes.

3. The method of claim 2, wherein said amount of transcripts is detected with a high density nucleic acid array.

5. The method of claim 1, wherein said biological samples are prepared by a homozygous knockout strategy.

6. The method of claim 1, wherein each of said biological samples is derived from one clone of said cells.

7. The method of claim 1, wherein said biological samples are prepared using cells representing different developmental, physiological or pathological status.

8. The method of claim 1, wherein said biological samples are prepared by stimulating cells with a combination of a plurality of hormones.

9. The method of claim 1, wherein said biological samples are prepared by transfecting cells with a combination of a plurality of vectors, said vectors being used by said cells as templates to transcribe a plurality of RNAs, each of said RNAs having a sequence complementary to one of said genes.

10. The method of claim 1, wherein said gene network causal models are generated and tested using the Linear Structure Relations (LISREL) process performed in a digital computer.

11. A method for detecting a functional mutation in a target up-stream regulatory gene comprising:

preparing a reference sample from reference cells having a wild-type up-stream regulatory gene corresponding to said target up-stream regulatory gene;

preparing a target sample from target cells suspected of having a mutation in said target up-stream regulatory gene, said target cells being otherwise substantially similar to said reference cells;

detecting the expression of a plurality of down-stream genes in said reference sample to obtain a reference expression pattern, said down-stream genes being up or down regulated by said wild-type up-stream regulatory gene;

detecting the expression of said plurality of down-stream genes in said target sample to obtain a target expression pattern; and

comparing said reference expression pattern with said target expression pattern to detect functional mutation in or inactivation of said target gene.

12. The method of claim 11, wherein said down-stream genes are transcriptionally regulated by said wild-type up-stream regulatory gene and said reference and target expression patterns are detected by measuring the amount of transcripts of said down-stream genes in said reference and target samples.

13. The method of claim 12, wherein said amount of transcripts is detected with a high density nucleic acid array.

14. The method of claim 11, wherein said reference and target expression patterns are detected by measuring the amount of protein products of said down-stream genes in said reference and target samples.

15. The method of claim 11 further comprising the steps of:

detecting expression of a plurality of control genes in said reference and target samples, said control genes being unresponsive to the function of said up-stream regulatory gene; and

comparing reference and target expression patterns of control genes to provide a baseline for detecting a significant difference in expression patterns.

16. The method of claim 11 further comprising the step of:

indicating a loss of wild-type function in said target gene if a significant number of said down regulated genes are expressed relatively higher in said target sample than in said reference sample or if a significant number of said up-regulated genes are expressed relatively lower in said target sample than in said reference sample.

17. The method of claim 11 further comprising the step of:

indicating a gain of function mutation in said target gene if a significant portion of said down regulated genes are expressed relatively lower in said target sample than in said reference sample or if a significant portion of said up-regulated genes are expressed relatively higher in said target sample than in said reference sample.

18. A method for determining the function of a sequence alteration in a target up-stream regulatory gene comprising the steps of:

preparing a reference sample from reference cells having a wild-type up-stream regulatory gene corresponding to said target up-stream regulatory gene;

preparing a target sample from target cells having said target up-stream regulatory gene, said target up-stream regulatory gene having said sequence alteration and said target cells being otherwise substantially similar to said reference cells;

detecting the expression of a plurality of down-stream genes in said reference sample to obtain a wild-type expression pattern, said down-stream genes being up or down regulated by said up-stream regulatory gene;

detecting the expression of said plurality of down-stream genes in said target sample to obtain a target expression pattern; and

comparing said reference expression pattern with said target expression pattern to determine the regulatory function of said sequence alteration.

19. The method of claim 18, wherein said down-stream genes are transcriptionally regulated by said up-stream regulatory gene and said reference and target expression patterns are detected by measuring the amount of transcripts of said down-stream genes in said reference and target samples.

20. The method of claim 19, wherein said amount of transcripts is detected with a high density nucleic acid array.

21. The method of claim 18, wherein said reference and target expression patterns are detected by measuring the amount of protein product of said down-stream genes in said reference and target samples.

22. The method of claim 18 further comprising the steps of:

detecting expression of a plurality of control genes in said reference and target sample, said control genes being unresponsive to the function of said up-stream regulatory gene; and

comparing reference and target expression patterns of control genes to provide a baseline for detecting a significant difference in expression pattern.

23. The method of claim 18 further comprising the steps of:

a) indicating that said sequence alteration is a loss of function mutation in said target gene if a significant portion of said down regulated genes are expressed relatively higher in said target sample than in said reference sample or if a significant portion of said up-regulated genes are expressed relatively lower in said target sample than in said reference sample;

b) indicating that said sequence alteration is a gain of function mutation in said target gene if a significant portion of said down regulated genes are expressed relatively lower in said target sample than in said reference sample or if a significant portion of said up-regulated genes are expressed relatively higher in said target sample than in said reference sample; and

c) indicating that said sequence alteration is a non functional polymorphism if said reference and target expression patterns are substantially similar.

24. The method of claim 23, wherein said steps (a), (b) and (c) are performed using a digital computer.

25. A method for determining genetic regulatory function of a target gene in a target cell type comprising the steps of:

preparing a reference sample from said target cell type having an expressed gene product of said target gene;

blocking the expression of said target gene in said target cell type to prepare a lack-of- function sample;

detecting the expression of at least 2,000 genes in said reference sample and in said lack-of-function sample to obtain a reference and lack-of-function expression pattern; and

comparing said reference expression pattern with said lack-of-function expression pattern to determine the regulatory function of said target gene.

26. The method of claim 25, wherein said reference and lack-of-function expression patterns are detected by measuring the amount of transcripts of said down-stream genes in said reference and target samples.

27. The method of claim 26, wherein said amount of transcripts is detected with a high density nucleic acid array.

28. The method of claim 25, wherein the expression of said target gene is blocked in said loss of function assay by introducing an antisense oligonucleotide.

29. A method for detecting a p53 gene functional mutation in target cells comprising the steps of:

preparing a reference sample from reference cells having a wild-type p53 gene, said reference cells being otherwise substantially similar to said target cells;

detecting the expression of a plurality of down-stream genes in said reference cells and said target cells to obtain a target expression pattern, said down-stream genes being up- or down-regulated by said wild-type p53 gene; and

comparing said reference expression pattern with said target expression pattern to detect said p53 functional mutation.

30. The method of claim 29, wherein said down-stream genes are transcriptionally regulated by said wild-type p53 gene and the expression of said down-stream genes is detected by measuring the amount of transcripts of said down-stream genes in said reference and target cells.

31. The method of claim 30, wherein said amount of transcripts is measured with high density nucleic acid array.

32. The method of claim 30, wherein said down-stream genes comprise p53 up-regulated gadd45, cyclin G, p21wafl, Bax, IGF-BP3 and Thrombospondin genes and p53 down-regulated c-myc and PCNA genes.

33. The method of claim 32 further comprising the step of:

indicating a loss of function mutation in said p53 gene if the expression of said p53 up-regulated genes is at least five times less in said target cells than in said reference cells or if the expression of said p53 down-regulated genes is at least five times more in said target cells than in said reference cells.

34. An in-cell functional assay for a p53 sequence alteration comprising the steps of:

preparing a target sample from target cells having said p53 sequence alteration;

preparing a reference sample from reference cells having a wild-type p53 gene, said reference cells being otherwise substantially similar to said target cells;

detecting the expression of a plurality of down-stream genes in said reference cells to obtain a reference expression pattern and in said target cells to obtain a target expression pattern, said down-stream genes being up- or down-regulated by said wild-type p53 gene; and

comparing said reference expression pattern with said target expression pattern to determine the function of said p53 sequence alteration.

35. The method of claim 34, wherein said down-stream genes are transcriptionally regulated by said wild-type p53 gene and the expression of said down-stream genes is detected by measuring the amount of transcripts of said down-stream genes in said reference and target cells.

36. The method of claim 35, wherein said amount of transcripts is measured with a high density nucleic acid array.

37. The method of claim 35, wherein said down-stream genes comprise p53 up regulated gadd45, cyclin G, p21wafl, Bax, IGF-BP3 and Thrombospondin genes and p53 down regulated c-myc and PCNA genes.

38. The method of claim 35 further comprising the steps of:

indicating that said p53 sequence alteration is a loss of wild-type function mutation if the expression of said p53 up regulated genes is at least five times less in said target cells than in said reference cells or if the expression of said p53 down regulated genes is at least five times more in said target cells than in said reference cells.

39. A device for detecting a functional mutation in a target regulatory gene comprising a high density nucleic acid array, said nucleic acid array comprising sequences complementary to subsequences of a plurality of down-stream regulatory

genes, said regulatory genes being up or down regulated by a wild-type gene corresponding to said target regulatory gene.

40. The device of claim 39, wherein said high density nucleic acid array further comprising a tiling sequences for determining sequence alteration in said target regulatory gene.

41. A method of detecting a putative mutated gene in a diseased cell comprising the steps of:

preparing a reference sample from a normal cell and a target sample from said diseased cell;

detecting the expression of at least 100 genes of interest in both said reference sample and said target sample;

indicating those genes whose expression is either increased or decreased in said diseased cell as affected genes;

indicating the up-stream gene of said affected genes as said putative mutated gene.

42. The method of claim 41, wherein said putative mutated gene is an up-stream gene transcriptionally regulating said affected genes and the expression of said genes is detected by measuring the amount of transcripts of said genes.

43. The method of claim 42, wherein said amount of transcripts is determined with a high density nucleic acid array.

44. A method for analyzing gene expression data in a computer comprising:

inputing a plurality of expression data reflecting the expression of at least 5 genes in a plurality of biological samples;

correlating said expression data among said genes;

analyzing said correlation to define a regulatory relationship among said genes.

45. A method for detecting a mutation in a target gene using a computer comprising:

inputting target expression data of a plurality of genes in a target sample containing said target gene, said genes being regulated by said target gene;

inputting wild-type expression data of said plurality of genes in a wild-type sample containing a wild-type gene corresponding to said target gene;

comparing the target and wild-type expresssion data to detect mutation in said target gene.

46. A method of determining loss of function of a nucleic acid encoding a regulatory molecule in a test cell comprising:

selecting a first nucleic acid molecule encoding a regulatory molecule;

selecting a set of second nucleic acid molecules whose expression is induced or repressed by the regulatory molecule in normal cells;

hybridizing a transcription indicator of a test cell to a set of nucleic acid probes, wherein the transcription indicator is selected from the group consisting of mRNA, cDNA and cRNA, wherein each member of the set of nucleic acid probes comprises a portion of a nucleic acid molecule which is a member of the set of second nucleic acid molecules;

detecting the amount of transcription indicator which hybridizes to each of said set of nucleic acid probes;

identifying a test cell as having lost function of the regulatory molecule if (1) hybridization of the transcription indicator of the test cell to a probe which comprises a portion of a nucleic acid which is induced by the regulatory molecule is lower than hybridization using a transcription indicator from a normal cell, or (2) hybridization of the transcription indicator of the test cell to a probe which comprises a portion of a nucleic acid which is repressed by the regulatory molecule is higher than hybridization using a transcription indicator from a normal cell.

47. The method of claim 46 wherein the regulatory molecule is p53.

48. The method of claim 46wherein the test cell is a breast cell.

49. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 4 genes which are activated or repressed by p53.

50. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 10 genes which are activated or repressed by p53.

51. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 20 genes which are activated or repressed by p53.

52. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 30 genes which are activated or repressed by p53.

53. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 100 genes which are activated or repressed by p53.

54. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 250 genes which are activated or repressed by p53.

55. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 300 genes which are activated or repressed by p53.

56. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 400 genes which are activated or repressed by p53.

57. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 500 genes which are activated or repressed by p53.

58. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 750 genes which are activated or repressed by p53.

59. The method of claim 46 wherein the set of nucleic acid probes comprises nucleic acid sequences which comprise a portion of at least 1000 genes which are activated or repressed by p53.

60. The method of claim 46 wherein the nucleic acids which each comprise a portion of a gene which is activated or repressed by p53 are selected from those shown in Table 3.

61. The method of claim 46 wherein the nucleic acid probes are attached to a solid support.

62. The method of claim 46 wherein the nucleic acid probes are arranged in an array.

63. The method of claim 62 wherein the array comprises nucleic acid probes which are portions of at least 250 genes which are either p53-induced or p53-repressed.

64. The method of claim 62 wherein the array comprises nucleic acid probes which are portions of at least 6000 different genes.

65. The method of claim 46 wherein at least one of the nucleic acid probes comprises a portion of each of: Cyclin G, GADD45, IGF-BP3, $p21^{WAF1/CIP1}$, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

66. The method of claim 46 wherein at least one of the nucleic acid probes comprises a portion of each of: Bax, Cyclin G, GADD45, IGF-BP3, $p21^{WAF1/CIP1}$, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

67. The method of claim 46 further comprising the step of:

determining the sequence of p53 genes in the test cell to confirm the p53 status of the cell.

68. The method of claim 46 wherein a test cell is identified as p53-negative if hybridization is at least 3-fold different between compared samples.

69. The method of claim 46 wherein a test cell is identified as p53-negative if hybridization is at least 5-fold different between compared samples.

70. The method of claim 46 wherein a test cell is identified as p53-negative if hybridization is at least 10-fold different between compared samples.

71. A method of diagnosing neoplasia of a test cell comprising:

hybridizing a transcription indicator of a test cell to a set of nucleic acid probes, wherein the transcription indicator is selected from the group consisting of mRNA, cDNA and cRNA, wherein the set of nucleic acid probes comprises at least one nucleic acid molecule which is a portion of a gene which is activated by or repressed by p53;

detecting the amount of transcription indicator which hybridizes to each of said set of nucleic acid probes;

identifying a test cell as neoplastic if (1) hybridization of the transcription indicator of the test cell to a probe which is a p53-activated gene is lower than hybridization using a transcription indicator from a normal cell, or (2) hybridization of the transcription indicator of the test cell to a probe which a p53-repressed gene is higher than hybridization using a transcription indicator from a normal cell.

72. The method of claim 71 wherein the test cell is a breast cell.

73. The method of claim 71 wherein at least 4 of said probes comprise portions of genes which are p53-activated or p53-repressed.

74. The method of claim 71 wherein at least 10 of said probes comprise portions of genes which are p53-activated or p53-repressed.

75. The method of claim 71 wherein at least 20 of said probes comprise portions of genes which are p53-activated or p53-repressed.

76. The method of claim 71 wherein at least 30 of said probes comprise portions of genes which are p53-activated or p53-repressed.

77. The method of claim 71 wherein at least 50 of said probes comprise portions of genes which are p53-activated or p53-repressed.

78. The method of claim 71 wherein at least 75 of said probes comprise portions of genes which are p53-activated or p53-repressed.

79. The method of claim 71 wherein at least 100 of said probes comprise portions of genes which are p53-activated or p53-repressed.

80. The method of claim 71 wherein at least 250 of said probes comprise portions of genes which are p53-activated or p53-repressed.

81. The method of claim 71 wherein at least 300 of said probes comprise portions of genes which are p53-activated or p53-repressed.

82. The method of claim 71 wherein at least 500 of said probes comprise portions of genes which are p53-activated or p53-repressed.

83. The method of claim 71 wherein at least 750 of said probes comprise portions of genes which are p53-activated or p53-repressed.

84. The method of claim 71 wherein at least 1000 of said probes comprise portions of genes which are p53-activated or p53-repressed.

85. The method of claim 71 wherein the nucleic acid probes are attached to a solid support.

86. The method of claim 71 wherein the nucleic acid probes are arranged in an array.

87. The method of claim 86 wherein the array comprises nucleic acid probes which are portions of at least 250 different genes.

88. The method of claim 71 wherein the array comprises nucleic acid probes which are portions of at least 6000 different genes.

89. The method of claim 71 wherein at least one of the nucleic acid probes comprises a portion of each of: Bax, Cyclin G, GADD45, IGF-BP3, $p21^{WAF1/CIP1}$, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

90. The method of claim 71 wherein at least one of the nucleic acid probes comprises a portion of each of: Cyclin G, GADD45, IGF-BP3, $p21^{WAF1/CIP1}$, Thrombospondin, C-myc, and PCNA, as defined in Table 2.

91. The method of claim 71 further comprising the step of:

determining the sequence of p53 genes in the test cell to determine the p53 genotypic status of the cell.

92. The method of claim 71 wherein a test cell is identified as neoplastic if hybridization is at least 3-fold different between compared samples.

93. The method of claim 71 wherein a test cell is identified as neoplastic if hybridization is at least 5-fold different between compared samples.

94. The method of claim 71 wherein a test cell is identified as neoplastic if hybridization is at least 10-fold different between compared samples.

95. A method of identifying anti-cancer drugs, comprising the step of:

selecting a protein whose mRNA is induced in tumor cells;

contacting a test compound with the selected protein;